

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Beaudry, Gary A.
Maddon, Paul J.
- (ii) TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.24
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/485,163
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
- (viii) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 278-0400
(B) TELEFAX: (212) 391-0525
(C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: homo sapien
(G) CELL TYPE: lymphocyte
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Applicants : Gary Beaudry and
Paul J. Maddon
Serial No. : 08/485,163
Filed : June 7, 1995
Exhibit A

Phe Glu Arg Lys Cys Cys Val Gln Cys Pro Pro Cys Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1796 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(G) CELL TYPE: Lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAAGCCCAGA GCCCTGCCAT TTCTGTGGGC TCAGGTCCCT ACTGCTCAGC CCCTTCCTCC 60
CTCGGCAAGG CCACAATGAA CCGGGGAGTC CCTTTTAGGC ACTTGCTTCT GGTGCTGCAA 120
CTGGCGCTCC TCCCAGCAGC CACTCAGGGA AAGAAAGTGG TGCTGGCAA AAAAGGGAT 180
ACAGTGGAAC TGACCTGTAC AGCTTCCCAG AAGAAGAGCA TACAATTCCA CTGGAAAAAC 240
TCCAACCAGA TAAAGATTCT GGGAAATCAG GGCTCCTTCT TAACTAAAGG TCCATCCAAG 300
CTGAATGATC GCGCTGACTC AAGAAGAAGC CTTTGGGACC AAGGAAACTT CCCCTGATC 360
ATCAAGAAC TTAAGATAGA AGACTCAGAT ACTTACATCT GTGAAGTGGA GGACCAGAAG 420
GAGGAGGTGC AATTGCTAGT GTTCGGATTG ACTGCCAACT CTGACACCCA CCTGCTTCAG 480
GGGCAGAGCC TGACCCCTGAC CTTGGAGAGC CCCCTGGTA GTAGCCCTC AGTGAATGT 540
AGGAGTCCAA GGGTAAAAAA CATAACAGGGG GGGAAAGACCC TCTCCGTGTC TCAGCTGGAG 600
CTCCAGGATA GTGGCACCTG GACATGCACT GTCTTGCAGA ACCAGAAGAA GGTGGAGTTC 660
AAAATAGACA TCGTGGTGCT AGCTTCGAG CGCAAATGTT GTGTCGAGTG CCCACCGTGC 720
CCAGGTAAGC CAGCCCAGGC CTCGCCCTCC AGCTCAAGGC GGGACAGGTG CCCTAGAGTA 780
GCCTGCATCC AGGGACAGGC CCCAGCTGGG TGCTGACACG TCCACCTCCA TCTCTTCCTC 840
AGCACCACCT GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CCAAAACCCA AGGACACCC 900
CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC ACGAAGACCC 960
CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG CATAATGCCA AGACAAAGCC 1020
ACGGGAGGAG CAGTTCAACA GCACGTTCCG TGTGGTCAGC GTCCTCACCG TTGTGCACCA 1080
GGACTGGCTG AACGGCAAGG AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCCAGCCCC 1140

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CATCGAGAAA ACCATCTCCA AAACCAAAGG TGGGACCCGC GGGGTATGAG GGCCACATGG	1200
ACAGAGGCCG GCTCGGCCA CCCTCTGCC C TGGGAGTGAC CGCTGTGCCA ACCTCTGTCC	1260
CTACAGGGCA GCCCCGAGAA CCACAGGTGT ACACCCTGCC CCCATCCCAG GAGGAGATGA	1320
CCAAGAACCA GGTCAGCCTG ACCTGCCTGG TCAAAGGCTT CTACCCCAGC GACATGCCG	1380
TGGAGTGGGA GAGCAATGGG CAGCCGGAGA ACAACTACAA GACCACACCT CCCATGCTGG	1440
ACTCCGACGG CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC AGGTGGCAGC	1500
AGGGGAAC TG CTTCTCATGC TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGCAGA	1560
AGAGCCTCTC CCTGTCTCCG GGTAAATGAG TGCCACGGCC GGCAAGCCCC CGCTCCCCAG	1620
GCTCTCGGGG TCGCGTGAGG ATGCTTGGCA CGTACCCCGT GTACATACTT CCCAGGCACC	1680
CAGCATGGAA ATAAAGCACC CAGCGCTGCC CTGGGCCCCCT GCGAGACTGT GATGGTTCTT	1740
TCCGTGGGTC AGGCCGAGTC TGAGGCCTGA GTGGCATGAG GGAGGCAGAG TGGGTC	1796

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homo sapien
(G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1 5 10 15

Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
20 25 30

Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
35 40 45

Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
50 55 60

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65 70 75 80

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Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
85 90 95

Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
100 105 110

Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
115 120 125

Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
130 135 140

Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
145 150 155 160

Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
165 170 175

Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
180 185 190

Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Glu Arg Lys Cys
195 200 205

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
210 215 220

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
225 230 240

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
245 250 255

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
260 265 270

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
275 280 285

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
290 295 300

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
305 310 315 320

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cont

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
325 330 335

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
340 345 350

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
355 360 365

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
370 375 380

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
385 390 395 400

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
405 410 415

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
420 425 430

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapien
- (G) CELL TYPE: lymphocyte

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAGCCCAGA	GCCCTGCCAT	TTCTGTGGGC	TCAGGTCCCT	ACTGCTCAGC	CCCTTCCCTCC	60
CTCGGCAAGG	CCACAATGAA	CCGGGGAGTC	CCTTTTAGGC	ACTTGCTTCT	GGTGCTGCAA	120
CTGGCGCTCC	TCCCCAGCAGC	CACTCAGGGGA	AAGAAAAGTGG	TGCTGGGCAA	AAAAGGGGAT	180
ACAGTGGAAC	TGACCTGTAC	AGCTTCCCAG	AAGAAGAGCA	TACAATTCCA	CTGGAAAAAC	240
TCCAACCAGA	TAAAGATTCT	GGGAAATCAG	GGCTCCTTCT	TAAC TAAAGG	TCCATCCAAG	300
CTGAATGATC	GCGCTGACTC	AAGAAGAAGC	CTTTGGGACC	AAGGAAACTT	CCCCCTGATC	360

ATCAAGAAC TTAAGATAGA AGACTCAGAT ACTTACATCT GTGAAGTGG A GGACCAGAAG 420
GAGGAGGTGC AATTGCTAGT GTTCGGATTG ACTGCCAACT CTGACACCCA CCTGCTTCAG 480
GGGCAGAGCC TGACCCCTGAC CTTGGAGAGC CCCCCCTGGTA GTAGCCCCTC AGTGCAATGT 540
AGGAGTCCAA GGGGTAAAAA CATACAGGGG GGGAAAGACCC TCTCCGTGTC TCAGCTGGAG 600
CTCCAGGATA GTGGCACCTG GACATGCACT GTCTTGAGA ACCAGAAGAA GGTGGAGTT 660
AAAATAGACA TCGTGGTGCT AGCTTCGCC TCCACCAAGG GCCCATCGGT CTTCCCCCTG 720
GCGCCCTGCT CCAGGAGCAC CTCCGAGAGC ACAGCCGCC TGGGCTGCCT GGTCAAGGAC 780
TACTTCCCCG AACCGGTGAC GGTGTCGTGG AACTCAGGCG CTCTGACCAG CGGCAGTCAC 840
ACCTTCCCAG CTGTCCTACA GTCCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG 900
CCCTCCAGCA ACTTCGGCAC CCAGACCTAC ACCTGCAACG TAGATCACAA GCCCAGCAAC 960
ACCAAGGTGG ACAAGACAGT TGGTGAGAGG CCAGCTCAGG GAGGGAGGGT GTCTGCTGG 1020
AGCCAGGCTC AGCCCTCCTG CCTGGACGCA CCCCCGGCTGT GCAGCCCCAG CCCAGGGCAG 1080
CAAGGCAGGC CCCATCTGTC TCCTCACCCG GAGGCCTCTG CCCGCCCCAC TCATGCTCAG 1140
GGAGAGGGTC TTCTGGCTTT TTCCACCAAGG CTCCAGGCAG GCACAGGCTG GGTGCCCCTA 1200
CCCCAGGGCC TTCACACACA GGGGCAGGTG CTTGGCTCAG ACCTGCCAAA AGCCATATCC 1260
GGGAGGACCC TGCCCTGAC CTAAGCCGAC CCCAAAGGCC AAACGTCCA CTCCCTCAGC 1320
TCGGACACCT TCTCTCCTCC CAGATCCGAG TAACTCCCAA TCTTCTCTCT GCAGAGCGCA 1380
AATGTTGTGT CGAGTGCCC CCGTGCCAG GTAAGCCAGC CCAGGCCTCG CCCTCCAGCT 1440
CAAGGCAGGA CAGGTGCCCT AGAGTAGCCT GCATCCAGGG ACAGGCCCA GCTGGGTGCT 1500
GACACGTCCA CCTCCATCTC TTCCCTCAGCA CCACCTGTGG CAGGACCGTC AGTCTTCCTC 1560
TTCCCCCCAA AACCCAAGGA CACCCCTCATG ATCTCCCGGA CCCCTGAGGT CACGTGCGTG 1620
GTGGTGGACG TGAGCCACGA AGACCCCGAG GTCCAGTTCA ACTGGTACGT GGACGGCGTG 1680
GAGGTGCATA ATGCCAAGAC AAAGCCACGG GAGGAGCAGT TCAACAGCAC GTTCCGTGTC 1740
GTCAGCGTCC TCACCGTTGT GCACCAAGGAC TGGCTGAACG GCAAGGGAGTA CAAAGTGCAAG 1800
GTCTCCAACA AAGGCCTCCC AGCCCCATC GAGAAAACCA TCTCCAAAAC CAAAGGTGGG 1860
ACCCGCGGGG TATGAGGGCC ACATGGACAG AGGCCGGCTC GGCCCACCCCT CTGCCCTGGG 1920
AGTGACCGCT GTGCCAACCT CTGTCCTAC AGGGCAGCCC CGAGAACCCAC AGGTGTACAC 1980
CCTGCCCTCCA TCCCGGGAGG AGATGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA 2040
AGGCTTCTAC CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC CGGAGAACAA 2100

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CTACAAGACC ACACCTCCC	TGCTGGACTC CGACGGCTCC	TTCTTCCTCT ACAGCAAGCT	2160
CACCGTGGAC AAGAGCAGGT	GGCAGCAGGG GAACGTCTTC	TCATGCTCCG TGATGCATGA	2220
GGCTCTGCAC AACCACTACA	CGCAGAAGAG CCTCTCCCTG	TCTCCGGGTA AATGAGTGCC	2280
ACGGCCGGCA AGCCCCCGCT	CCCCAGGCTC TCGGGGTCGC	GTGAGGATGC TTGGCACGTA	2340
CCCCGTGTAC ATACTTCCC	GGCACCCAGC ATGGAAATAA	AGCACCCAGC GCTGCCCTGG	2400
GCCCCTGCGA GACTGTGATG	GTTCTTCCG TGGGTCAGGC	CGAGTCTGAG GCCTGAGTGG	2460
CATGAGGGAG GCAGAGTGGG	TC		2482

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: homo sapien
 - (G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1 5 10 15

Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
20 25 30

Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
35 40 45

Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
50 55 60

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65 70 75 80

Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
85 90 95

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Cont

Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
100 105 110

Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
115 120 125

Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
130 135 140

Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
145 150 155 160

Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
165 170 175

Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
180 185 190

Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Ala Ser Thr Lys
195 200 205

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
210 215 220

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
225 230 235 240

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
245 250 255

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
260 265 270

Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
275 280 285

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg
290 295 300

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
305 310 315 320

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
325 330 335

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Cont'

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
340 345 350

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
355 360 365

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
370 375 380

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
385 390 395 400

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
405 410 415

Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
420 425 430

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
435 440 445

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
450 455 460

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
465 470 475 480

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
485 490 495

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
500 505 510

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
515 520 525

Gly Lys
530

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapien
(G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAAGCCCAGA GCCCTGCCAT TTCTGTGGGC TCAGGGTCCCT ACTGCTCAGC CCCTTCCTCC 60
CTCGGCAAGG CCACAATGAA CGGGGGAGTC CCTTTAGGC ACTTGCTTCT GGTGCTGCAA 120
CTGGCGCTCC TCCCAGCAGC CACTCAGGGA AAGAAAAGTGG TGCTGGCAA AAAAGGGGAT 180
ACAGTGGAAC TGACCTGTAC AGCTTCCCAG AAGAAGAGCA TACAATTCCA CTGGAAAAAC 240
TCCAACCAGA TAAAGATTCT GGGAAATCAG GGCTCCTTCT TAACTAAAGG TCCATCCAAG 300
CTGAATGATC GCGCTGACTC AAGAAGAAGC CTTTGGGACC AAGGAAACTT CCCCCTGATC 360
ATCAAGAACAT TTAAGATAGA AGACTCAGAT ACTTACATCT GTGAAGTGGA GGACCAGAAG 420
GAGGAGGTGC AATTGCTAGT GTTCGGATTG ACTGCCAACT CTGACACCCA CCTGCTTCAG 480
GGGCAGAGCC TGACCTGAC CTTGGAGAGC CCCCCTGGTA GTAGCCCTC AGTGAATGT 540
AGGAGTCCAA GGGTAAAAAA CATAACAGGGG GGGAAAGACCC TCTCCGTGTC TCAGCTGGAG 600
CTCCAGGATA GTGGCACCTG GACATGCACT GTCTTGCAGA ACCAGAAGAA GGTGGAGTTC 660
AAAATAGACA TCGTGGTGCT AGCTTCACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 720
CCATCTGATG AGCAGTTGAA ATCTGGAAC GCCTCTGTTG TGTGCCTGCT GAATAACTTC 780
TATCCCAGAG AGGCCAAAGT ACAGTGGAAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 840
CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCCTG 900
ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 960
GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGTAGAG GGAGAAGTGC 1020
CCCCACCTGC TCCTCAGTTC CAGCCTGACC CCCTCCCATC CTTTGGCCTC TGACCCCTTT 1080
TCCACAGGGG ACCTACCCCT ATTGCGGTCC TCCAAGCTCA TCTTCACCT CACCCCCCTC 1140
CTCCTCCTT 1149

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: homo sapien
(G) CELL TYPE: lymphocyte

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
1 5 10 15

Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
20 25 30

Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
35 40 45

Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
50 55 60

Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
65 70 75 80

Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
85 90 95

Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
100 105 110

Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
115 120 125

Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
130 135 140

Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
145 150 155 160

Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
165 170 175

Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
180 185 190

Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Thr Val Ala Ala
195 200 205

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Cont.

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
210 215 220

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
225 230 235 240

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
245 250 255

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
260 265 270

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
275 280 285

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
290 295 300

Phe Asn Arg Gly Glu Cys
305 310

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: synthetic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- (G) CELL TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACACAACAT TTGCGCTCGA AAGCTAGCAC CACG

34

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: synthetic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(G) CELL TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGCCCTTGG TGGAGGCAGA AGCTAGCACC ACG

33

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: synthetic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(G) CELL TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATGGTGCAG CCACAGTGAA AGCTAGCACC ACG

33

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